



Ms. Delora Dillard, OIPE

FROM: Anne-Marie Corrigan, STIC  
571-272-2501

Per your request, please find re-run of latest raw sequence listing (RSL) of 10/658355.  
Total pages: 9, includes cover sheet.

Thank you.

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STIC Biotechnology Systems BranchRAW SEQUENCE LISTING  
ERROR REPORT*re-run*

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/658,355A  
Source: 1/FW0  
Date Processed by STIC: 3/16/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE  
APPLICANT, WITH A NOTICE TO COMPLY or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A  
NOTICE TO COMPLY  
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT  
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:  
<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.  
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.  
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated address:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

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Revised 01/24/05.

## Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTED CORRECTIONSERIAL NUMBER:

101658,355A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS WHICH WERE INSERTED BY PTO SOFTWARE

1  **Wrapped Nucleic  
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

3  **Misaligned Amino  
Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4  **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6  **PatentIn 2.0  
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7  **Skipped Sequences  
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(x) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8  **Skipped Sequences  
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

9  **Use of n's or Xaa's  
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  **Invalid <213>  
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence

11  **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29634-32) (Sec. 1.823 of Sequence Rules)

12  **PatentIn 2.0  
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

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IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004  
TIME: 07:58:57

Input Set: D:\923seq.002  
Output Set: N:\CRF4\03162004\J658355A.raw

3 <110> APPLICANT: Gantier, Rene  
4 Guyon, Thierry  
5 Hugo, Cruz Ramos  
6 Vega, Manuel  
7 Drittanti, Lila  
9 <120> TITLE OF INVENTION: Rational Directed Protein Evolution Using Two Dimensional  
10 Rational  
11 Mutagenesis Scanning  
13 <130> FILE REFERENCE: 38751-923  
15 <140> CURRENT APPLICATION NUMBER: US/10/658,355A  
16 <141> CURRENT FILING DATE: 2003-09-08  
18 <150> PRIOR APPLICATION NUMBER: 60/457,063  
19 <151> PRIOR FILING DATE: 2003-03-21  
21 <150> PRIOR APPLICATION NUMBER: 60/410,258  
22 <151> PRIOR FILING DATE: 2002-09-09  
24 <160> NUMBER OF SEQ ID NOS: 501  
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply  
Corrected Diskette Needed  
(Pg. 1 - 6)

## ERRORED SEQUENCES

7445 <210> SEQ ID NO: 182  
7446 <211> LENGTH: 55  
7447 <212> TYPE: DNA  
7448 <213> ORGANISM: Artificial Sequence  
7450 <220> FEATURE:  
7451 <223> OTHER INFORMATION: EcoRI Forward Primer  
7453 <400> SEQUENCE: 182  
E--> 7454 ~~gcgttatgatttatggatgttggaaatccgttatgcggatattttatccat~~ ttacg  
7455 (55) ~~gcgttatgatttatggatgttggaaatccgttatgcggatattttatccat~~ ttacg  
7457 <210> SEQ ID NO: 183  
7458 <211> LENGTH: 55  
7459 <212> TYPE: DNA  
7460 <213> ORGANISM: Artificial Sequence  
7462 <220> FEATURE:  
7463 <223> OTHER INFORMATION: EcoRI Reverse Primer  
7465 <400> SEQUENCE: 183  
E--> 7466 ~~ccttaaggagaaaataccgca tcaggaaattccaaacatccataataaattatcata~~ caggc  
7467 (55) ~~ccttaaggagaaaataccgca tcaggaaattccaaacatccataataaattatcata~~ caggc  
7469 <210> SEQ ID NO: 184  
7470 <211> LENGTH: 35  
7471 <212> TYPE: DNA  
7472 <213> ORGANISM: Artificial Sequence

please see  
item # 1  
on error  
summary  
sheet.

55

insert  
here

55  
insert  
here

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/658,355ADATE: 03/16/2004  
TIME: 07:58:58Input Set : D:\923seq.002  
Output Set: N:\CRF4\03162004\J658355A.rawSAME  
errors

7474 <220> FEATURE:  
 7475 <223> OTHER INFORMATION: Seq ClaI Forward Primer  
 7477 <400> SEQUENCE: 184  
 E--> 7478 ctgtatatac accgcgtac atatgattga catgc  
 7479 35  
 7481 <210> SEQ ID NO: 185  
 7482 <211> LENGTH: 31  
 7483 <212> TYPE: DNA  
 7484 <213> ORGANISM: Artificial Sequence  
 7486 <220> FEATURE:  
 7487 <223> OTHER INFORMATION: Seq ClaI Reverse Primer  
 7489 <400> SEQUENCE: 185  
 E--> 7490 taaggataa taccgcgcata catagcagaa c  
 7491 31  
 7493 <210> SEQ ID NO: 186  
 7494 <211> LENGTH: 18  
 7495 <212> TYPE: DNA  
 7496 <213> ORGANISM: Artificial Sequence  
 7498 <220> FEATURE:  
 7499 <223> OTHER INFORMATION: Seq Forward Primer  
 7501 <400> SEQUENCE: 186  
 E--> 7502 cctgtatgaa gaggact  
 7503 18  
 7505 <210> SEQ ID NO: 187  
 7506 <211> LENGTH: 18  
 7507 <212> TYPE: DNA  
 7508 <213> ORGANISM: Artificial Sequence  
 7510 <220> FEATURE:  
 7511 <223> OTHER INFORMATION: Seq Reverse Primer  
 7513 <400> SEQUENCE: 187  
 E--> 7514 ccaagcagca gatgagtc  
 7515 18  
 7517 <210> SEQ ID NO: 188  
 7518 <211> LENGTH: 31  
 7519 <212> TYPE: DNA  
 7520 <213> ORGANISM: Artificial Sequence  
 7522 <220> FEATURE:  
 7523 <223> OTHER INFORMATION: IFN alpha-2b 5' Primer  
 7525 <400> SEQUENCE: 188  
 E--> 7526 tcgtctgcaa gtcagaagctgc tctgtgggc-f-g  
 7527 31  
 7529 <210> SEQ ID NO: 189  
 7530 <211> LENGTH: 48  
 7531 <212> TYPE: DNA  
 7532 <213> ORGANISM: Artificial Sequence  
 7534 <220> FEATURE:  
 7535 <223> OTHER INFORMATION: IFN alpha-2b 3' Primer  
 7537 <400> SEQUENCE: 189  
 E--> 7538 gctctagatc attccttact tottaaaactt ttttgcaagt ttgttgcac

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/658,355ADATE: 03/16/2004  
TIME: 07:58:58Input Set : D:\923seq.002  
Output Set: N:\CRF4\03162004\J658355A.raw

Same errors

7539. 48  
 7541 <210> SEQ ID NO: 190  
 7542 <211> LENGTH: 36  
 7543 <212> TYPE: DNA  
 7544 <213> ORGANISM: Artificial Sequence  
 7546 <220> FEATURE:  
 7547 <223> OTHER INFORMATION: IFN alpha-2b HindIII Primer  
 7549 <400> SEQUENCE: 190  
 E--> 7550 cccaaagctta tggccttgac ctttgcctta ctgggt 36  
 7551 36  
 7553 <210> SEQ ID NO: 191  
 7554 <211> LENGTH: 48  
 7555 <212> TYPE: DNA  
 7556 <213> ORGANISM: Artificial Sequence  
 7558 <220> FEATURE:  
 7559 <223> OTHER INFORMATION: IFN alpha-2b XbaI Primer  
 7561 <400> SEQUENCE: 191  
 E--> 7562 gctctagatc attccttact tcttaaactt tcttgcaagt ttgttgac 48  
 7563 48  
 7565 <210> SEQ ID NO: 192  
 7566 <211> LENGTH: 80  
 7567 <212> TYPE: DNA  
 7568 <213> ORGANISM: Artificial Sequence  
 7570 <220> FEATURE:  
 7571 <223> OTHER INFORMATION: IFN alpha-2b 80 bp 5' Primer  
 7573 <400> SEQUENCE: 192  
 E--> 7574 cccaaagctta tggccttgac ctttgcctta ctgggtggcc tctgggtct cagctgcaag 60  
 E--> 7575 80  
 E--> 7576 tcaagctgt ctgtgggctg 80  
 7578 <210> SEQ ID NO: 193  
 7579 <211> LENGTH: 20  
 7580 <212> TYPE: DNA  
 7581 <213> ORGANISM: Artificial Sequence  
 7583 <220> FEATURE:  
 7584 <223> OTHER INFORMATION: EMCV Forward Primer  
 7586 <400> SEQUENCE: 193  
 E--> 7587 cccctacatt gaggcatcca  
 7588 20  
 7590 <210> SEQ ID NO: 194  
 7591 <211> LENGTH: 21  
 7592 <212> TYPE: DNA  
 7593 <213> ORGANISM: Artificial Sequence  
 7595 <220> FEATURE:  
 7596 <223> OTHER INFORMATION: EMCV Reverse Primer  
 7598 <400> SEQUENCE: 194  
 E--> 7599 caggaggcagg acaagggtcac t  
 7600 21  
 7602 <210> SEQ ID NO: 195  
 7603 <211> LENGTH: 22

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004

TIME: 07:58:58

Input Set : D:\923seq.002  
Output Set: N:\CRF4\03162004\J658355A.rawSame  
errors

7604 <212> TYPE: DNA  
7605 <213> ORGANISM: Artificial Sequence  
7607 <220> FEATURE:  
7608 <221> NAME/KEY: misc feature  
7609 <222> LOCATION: 1; 22  
7610 <223> OTHER INFORMATION: EMCV Probe: n at position 1 is a 5-carboxyfluorescein  
7611 (FAM)-modified deoxycytidylate; n at position 22 is an N,N,N',N'-  
7612 tetramethyl-6-carboxyrhodamine (TAMRA)-modified deoxythymidylate.  
7614 <400> SEQUENCE: 195  
E--> 7615 naggcgtca agacccaaacc gcn  
7616 (22)  
8074 <210> SEQ ID NO: 208  
8075 <211> LENGTH: 41  
8076 <212> TYPE: DNA  
8077 <213> ORGANISM: Artificial Sequence  
8079 <220> FEATURE:  
8080 <223> OTHER INFORMATION: Oligonucleotide  
8082 <400> SEQUENCE: 208  
E--> 8083 aacatatgtg ttagatgtgcct caaaaccacaca gcctgggttag c  
8084 (41)  
8086 <210> SEQ ID NO: 209  
8087 <211> LENGTH: 46  
8088 <212> TYPE: DNA  
8089 <213> ORGANISM: Artificial Sequence  
8091 <220> FEATURE:  
8092 <223> OTHER INFORMATION: Oligonucleotide  
8094 <400> SEQUENCE: 209  
E--> 8095 aaggatccctc attccattact tctttaaactt tcttgcaagt ttgttg  
8096 (46)  
8098 <210> SEQ ID NO: 210  
8099 <211> LENGTH: 41  
8100 <212> TYPE: DNA  
8101 <213> ORGANISM: Artificial Sequence  
8103 <220> FEATURE:  
8104 <223> OTHER INFORMATION: Oligonucleotide  
8106 <400> SEQUENCE: 210  
E--> 8107 aacatatgtg ttagatgtgcct caaaaccacaca gcctgggttag c  
8108 (41)  
8110 <210> SEQ ID NO: 211  
8111 <211> LENGTH: 46  
8112 <212> TYPE: DNA  
8113 <213> ORGANISM: Artificial Sequence  
8115 <220> FEATURE:  
8116 <223> OTHER INFORMATION: Oligonucleotide  
8118 <400> SEQUENCE: 211  
E--> 8119 aaggatccctc attccattact tctttaaactt tcttgcaagt ttgttg  
8120 (46)  
19072 <210> SEQ ID NO: 500  
19073 <211> LENGTH: 46

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RAW SEQUENCE LISTING DATE: 03/16/2004  
PATENT APPLICATION: US/10/658,355A TIME: 07:58:59

Input Set : D:\923seq.002  
Output Set: N:\CRF4\03162004\J658355A.ZAW

19074 <212> TYPE: DNA  
19075 <213> ORGANISM: Artificial Sequence  
19077 <220> FEATURE:  
19078 <223> OTHER INFORMATION: primer reverse INFA-E159H  
19080 <400> SEQUENCE: 500  
E--> 19081 aaggatccctc attccttact tcttaaactg tgttgcaagt ttgttg  
19082 46  
19084 <210> SEQ ID NO: 501  
19085 <211> LENGTH: 46  
19086 <212> TYPE: DNA  
19087 <213> ORGANISM: Artificial Sequence  
19089 <220> FEATURE:  
19090 <223> OTHER INFORMATION: primer reverse INFA-E159Q  
19092 <400> SEQUENCE: 501  
E--> 19093 aaggatccctc attccttact tcttaaactc tgttgcaagt ttgttg  
19094 46

Some  
errors

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/658,355A

DATE: 03/16/2004

TIME: 07:59:00

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

L:7454 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:182  
L:7466 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:183  
L:7478 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:184  
L:7490 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:185  
L:7502 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:186  
L:7514 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:187  
L:7526 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:188  
L:7538 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:189  
L:7550 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:190  
L:7562 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:191  
L:7574 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:192  
M:254 Repeated in SeqNo=192  
L:7587 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:193  
L:7599 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:194  
L:7615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:195 after pos.:0  
L:7615 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:195  
L:8083 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:208  
L:8095 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:209  
L:8107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:210  
L:8119 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:211  
L:19081 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:500  
L:19093 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:501

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